

1009

OIEP

#2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,243

DATE: 12/03/2001

TIME: 11:52:03

Input Set : N:\Crf3\RULE60\09905243.txt

Output Set: N:\CRF3\12032001\I905243.raw

4 <110> APPLICANT: Taylor, Alexander H
 6 <120> TITLE OF INVENTION: Monoclonal Antibodies with Reduced
 7 Immunogenicity
 9 <130> FILE REFERENCE: P50770
 11 <140> CURRENT APPLICATION NUMBER: 09/905,243
 12 <141> CURRENT FILING DATE: 2001-07-16
 14 <150> PRIOR APPLICATION NUMBER: 09/300,970
 15 <151> PRIOR FILING DATE: 1999-04-28
 17 <160> NUMBER OF SEQ ID NOS: 97
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 429
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Pan troglodytes
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)...(429)
 30 <400> SEQUENCE: 1

31	atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg	48
32	Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
33	1 5 10 15	
35	gtc ctg tcc cag gtg cag ttg cag gag tgc ggc cca gga ctg gtg aag	96
36	Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
37	20 25 30	
39	cct tca cag acc ttg tcc ctg acc tgc gct gtg tct ggt ggc tcc atc	144
40	Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
41	35 40 45	
43	act agt gct tac tac tat tgg agc tgg atc cgc cag tca cca ggg aag	192
44	Thr Ser Ala Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys	
45	50 55 60	
47	gga ctg gag tgg att ggg agt atc tat tat agt ggg acc att ttc tcc	240
48	Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser	
49	65 70 75 80	
51	aac cca tcc ctc aag agt cga gtc gcc atg tca gta ggc acg tcc aag	288
52	Asn Pro Ser Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys	
53	85 90 95	
55	acc cag ttc tcc ctg agc ttg agt tct gtg acc gcc gcg gac acg gcc	336
56	Thr Gln Phe Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala	
57	100 105 110	
59	gtg tac tac tgt gcg aga ggt ctg ctc ctc acc att gga ctg acc aac	384
60	Val Tyr Tyr Cys Ala Arg Gly Leu Leu Leu Thr Ile Gly Leu Thr Asn	
61	115 120 125	
63	tac tac ttt gac tac tgg ggc ccg gga acc ctg gtc acc gtc ttc	429
64	Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Phe	
65	130 135 140	
68	<210> SEQ ID NO: 2	
69	<211> LENGTH: 414	

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70 <212> TYPE: DNA
71 <213> ORGANISM: Pan troglodytes
73 <220> FEATURE:
74 <221> NAME/KEY: CDS
75 <222> LOCATION: (1)...(414)
77 <400> SEQUENCE: 2
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79 Met-Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
80 1 5 10 15
82 gtc ctg tcc cag gtg cag cta cag gag tgc ggc cca gga cta gtg aag      96
83 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
84 20 25 30
86 ccg tca cag acc ctg tcc ctc acc tgc ggt gtc tct ggt gcc tcc atc      144
87 Pro Ser Gln Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile
88 35 40 45
90 aat agt ggt gtt cat tac tgg gcc tgg ata cgc cag cct gca gga aag      192
91 Asn Ser Gly Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys
92 50 55 60
94 gga ctg gag tgg att ggc aat atc tat cat agt ggg agc gcc tac tac      240
95 Gly Leu Glu Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr
96 65 70 75 80
98 act cca tcc ctc gag agt cga gtc tcc atg tca ata gag acg tcc aag      288
99 Thr Pro Ser Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys
100 85 90 95
102 agc cag ttc ttc cta aac tta aat tct ctg acc gcc gcg gac acg gct      336
103 Ser Gln Phe Phe Leu Asn Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala
104 100 105 110
106 atc tat tat tgt gcg aga cga cat act tgc tca gac tac ttt gac ttt      384
107 Ile Tyr Tyr Cys Ala Arg Arg His Thr Ser Ser Asp Tyr Phe Asp Phe
108 115 120 125
110 tgg ggc cgc gga atc ctg gtc atc gtc tcc      414
111 Trp Gly Arg Gly Ile Leu Val Ile Val Ser
112 130 135
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 427
117 <212> TYPE: DNA
118 <213> ORGANISM: Pan troglodytes
120 <220> FEATURE:
121 <221> NAME/KEY: CDS
122 <222> LOCATION: (1)...(427)
124 <400> SEQUENCE: 3
125 atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc gaa gga      48
126 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Ala Val Leu Glu Gly
127 1 5 10 15
129 gtc cgt gca gac gtg cag ctg gtg cag tcc gga gca gag gtg aaa aag      96
130 Val Arg Ala Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
131 20 25 30
133 ccc ggg gag tct ctg aag atc tcc tgt aag gtc tct gga aat gaa ttt      144
134 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe

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135          35          40          45
137 acc aac tac tgg atc gcc tgg gtg cgc cag atg tcc ggg aaa ggc ctg 192
138 Thr Asn Tyr Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu
139          50          55          60
141 gag tgg atg ggg agc atc tat cct ggt gac tct gat acc aga tac aac 240
142 Glu Trp Met Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn
143 65          70          75          80
145 ccg tcc ttc caa ggc caa gtc acc ttt tca gcc gac aag tcc atc acc 288
146 Pro Ser Phe Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr
147          85          90          95
149 acc gcc tat ttg cag tgg agt agt ctg gag gcc tcg gac acc gcc atg 336
150 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met
151          100          105          110
153 tac tac tgt gcg agc cga aat cac ttt gtt ttc ggg gaa gtt att act 384
154 Tyr Tyr Cys Ala Ser Arg Asn His Phe Val Phe Gly Glu Val Ile Thr
155          115          120          125
157 act ttg acg gct ggg gcc agg gaa acc ctg ggt cac cgt ctc c 427
158 Thr Leu Thr Ala Gly Ala Arg Glu Thr Leu Gly His Arg Leu
159          130          135          140
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163 <211> LENGTH: 402
164 <212> TYPE: DNA
165 <213> ORGANISM: Pan troglodytes
167 <220> FEATURE:
168 <221> NAME/KEY: CDS
169 <222> LOCATION: (1)...(402)
171 <400> SEQUENCE: 4
172 ttg ggg ctc cgc tgg gtt ttc ctt gtt gct ttt tta gaa ggt gtc cag 48
173 Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly Val Gln
174 1          5          10          15
176 tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg 96
177 Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
178          20          25          30
180 ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc agt agg 144
181 Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg
182          35          40          45
184 agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg ggg tgg 192
185 Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp
186          50          55          60
188 ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg gac tca 240
189 Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser Asp Ser
190 65          70          75          80
192 gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat tca ctc 288
193 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
194          85          90          95
196 tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt tat tac 336
197 Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe Tyr Tyr
198          100          105          110
200 tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc cag gga 384

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201 Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly Gln Gly
202      115      120      125
204 acc ctg gtc acc gtc tcc 402
205 Thr Leu Val Thr Val Ser
206      130
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 408
211 <212> TYPE: DNA
212 <213> ORGANISM: Pan troglodytes
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (1)...(408)
218 <400> SEQUENCE: 5
219 atg gaa ttg ggg ctc cgc tgg gtt ttc ctt gtt gct ttt tta gaa ggt 48
220 Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly
221 1 5 10 15
223 gtc cag tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag 96
224 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
225 20 25 30
227 cct ggg ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc 144
228 Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
229 35 40 45
231 agt agg agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg 192
232 Ser Arg Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
233 50 55 60
235 gag tgg ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg 240
236 Glu Trp Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser
237 65 70 75 80
239 gac tca gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat 288
240 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
241 85 90 95
243 tca ctc tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt 336
244 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe
245 100 105 110
247 tat tac tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc 384
248 Tyr Tyr Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly
249 115 120 125
251 cag gga acc ctg gtc acc gtc tcc 408
252 Gln Gly Thr Leu Val Thr Val Ser
253 130 135
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 421
258 <212> TYPE: DNA
259 <213> ORGANISM: Pan troglodytes
261 <220> FEATURE:
262 <221> NAME/KEY: CDS
263 <222> LOCATION: (1)...(421)
265 <400> SEQUENCE: 6
266 atg atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa 48

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267 Met Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln
268 1 5 10 15
270 gga gtc tgt gca gag gtg cag ctg gtg cag tct gga gca gag gtg aaa 96
271 Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
272 20 25 30
274 aag ccc ggg gag tct ctg aag atc tcc tgt aag ggc tct gga tac agt 144
275 Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
276 35 40 45
278 ttt acc aac tac tgg atg ggc tgg gtg tgc cag atg ccc ggg aaa ggc 192
279 Phe Thr Asn Tyr Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly
280 50 55 60
282 ccg gag tgc atg ggg atc atc tat cct gat gac tct gat acc aga tac 240
283 Pro Glu Cys Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr
284 65 70 75 80
286 agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc 288
287 Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
288 85 90 95
290 agc acc gcc tac cta caa tgg agc aac ctg aag gcc tcg gac acc gcc 336
291 Ser Thr Ala Tyr Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala
292 100 105 110
294 ata tat tac tgt gcg aga tgt tat ggt tgg act act tgc gaa gct ttt 384
295 Ile Tyr Tyr Cys Ala Arg Cys Tyr Gly Trp Thr Thr Cys Glu Ala Phe
296 115 120 125
298 gat atc tgg ggc caa ggg aca atg gtc acc gtc tct t 421
299 Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
300 130 135 140
303 <210> SEQ ID NO: 7
304 <211> LENGTH: 417
305 <212> TYPE: DNA
306 <213> ORGANISM: Pan troglodytes
308 <220> FEATURE:
309 <221> NAME/KEY: CDS
310 <222> LOCATION: (1)...(417)
312 <400> SEQUENCE: 7
313 ttg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc 48
314 Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
315 1 5 10 15
317 cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag 96
318 Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
319 20 25 30
321 acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt 144
322 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
323 35 40 45
325 agt tac tac tgg agt tgg atc cgg cag ccc gcc ggg aag cga ctg gag 192
326 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu
327 50 55 60
329 tgg att ggg tat att tat tat agt ggg agt acc tac tac aac cca tcc 240
330 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
331 65 70 75 80

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/905,243

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